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OM nucleic - nucleic search, using sw model

Run on: June 6, 2001, 20:03:40 ; Search time 182.07 Seconds
(without alignments)
7055.888 Million cell updates/sec

Title: US-09-494-297-1

Perfect score: 2274
Sequence: 1 atgaaaaaacaagtttcc.....ggataaagaacatgactag 2274

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 470324 seqs, 282468253 residues

Total number of hits satisfying chosen parameters: 940648

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Pending Patents: NA, New: *
1: /cgml_7/ptodata/2/pna/US06_NEW_COMB.seq:*
2: /cgml_7/ptodata/2/pna/US07_NEW_COMB.seq:*
3: /cgml_7/ptodata/2/pna/US08_NEW_COMB.seq:*
4: /cgml_7/ptodata/2/pna/US09_NEW_COMB.seq:*
6: /cgml_7/ptodata/2/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2274	100.0	2274	US-09-494-297-1	Sequence 1, Appl1
2	720.8	31.7	2229	US-09-494-297-3	Sequence 3, Appl1
3	51.2	2.3	902	US-09-739-449-1979	Sequence 1929, Ap
4	49.4	2.2	780	US-09-739-449-451	Sequence 451, Ap
5	48.6	2.1	69513	US-60-248-823-16	Sequence 16, Appl
6	47.8	2.1	753	US-09-739-449-1234	Sequence 1234, Ap
7	47.4	2.1	834	US-09-739-449-2256	Sequence 2256, Ap
8	47.4	2.1	5897	US-08-956-171C-320	Sequence 320, App
9	47.2	2.1	1131	US-09-739-449-1953	Sequence 1953, Ap
10	46.4	2.0	723	US-09-739-449-8012	Sequence 8012, Ap
11	46.4	2.0	892	US-09-739-449-1335	Sequence 1335, Ap
12	46.4	2.0	2850	US-09-663-882-1	Sequence 1, Appl1
13	45.6	2.0	1250	US-09-739-449-1859	Sequence 1859, Ap
14	45.4	2.0	2841	US-08-956-171C-177	Sequence 177, App
15	44.8	2.0	1220	US-08-956-171C-918	Sequence 918, App
16	44.6	2.0	757	US-09-739-449-2286	Sequence 2286, Ap
17	44.4	2.0	1040	US-09-739-449-2287	Sequence 2287, Ap
18	44.4	1.9	787	US-09-739-449-2501	Sequence 2501, Ap
19	44.4	1.9	798	US-09-739-449-2641	Sequence 2641, Ap
20	43.8	1.9	786	US-09-739-449-1368	Sequence 1368, Ap
21	43.6	1.9	543	US-09-739-449-8029	Sequence 8029, Ap
22	43.6	1.9	856	US-09-833-343-74	Sequence 74, Appl
23	43.4	1.9	499	US-09-739-449-1332	Sequence 1332, Ap
24	43.4	1.9	776	US-09-739-449-2257	Sequence 2257, Ap
25	43.4	1.9	909	US-09-739-449-636	Sequence 636, App
26	43.4	1.9	117358	US-60-248-505-567	Sequence 567, App
27	42.8	1.9	1006	US-09-739-449-621	Sequence 621, App

28	42.8	1.9	43546	US-60-254-168-38	Sequence 38, Appl
29	42.6	1.9	780	US-09-739-449-778	Sequence 778, App
30	41.8	1.8	548	US-09-739-449-1457	Sequence 1457, Ap
31	41.8	1.8	403789	US-60-248-505-197	Sequence 197, App
32	41.6	1.8	681	US-09-739-449-2434	Sequence 2434, Ap
33	41.4	1.8	14333	US-08-956-171C-57	Sequence 57, Appl
34	41	1.8	385	US-09-737-223-6963	Sequence 6963, Ap
35	41	1.8	186647	US-60-248-823-22	Sequence 22, Appl
36	40.6	1.8	831	US-09-739-449-285	Sequence 285, App
37	40.6	1.8	1418	US-09-739-449-1613	Sequence 1613, Ap
38	40.2	1.8	664	US-09-739-449-739	Sequence 739, App
39	40	1.8	6373	US-08-956-171C-227	Sequence 227, App
40	39.8	1.8	6060	US-08-956-171C-534	Sequence 534, App
41	39.8	1.8	9821	US-08-956-171C-470	Sequence 470, App
42	39.8	1.8	15350	US-60-248-823-6	Sequence 6, Appl1
43	39.6	1.7	778	US-09-739-449-2435	Sequence 2435, Ap
44	39.6	1.7	1014	US-09-739-449-1697	Sequence 1697, Ap
45	39.4	1.7	849	US-09-739-449-1463	Sequence 1463, Ap

ALIGNMENTS

Copy

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RESULT 1
US-09-494-297-1
Sequence 1, Application US/09494297
GENERAL INFORMATION:
APPLICANT: PODIELSKI, ANDREAS
TITLE OF INVENTION: COLLAGEN-BINDING PROTEINS FROM STREPTOCOCCUS PYOGENES
FILE REFERENCE: P06628US0/BAS
CURRENT APPLICATION NUMBER: US/09/494, 297
CURRENT FILING DATE: 2000-01-31
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 2274
TYPE: DNA
ORGANISM: Streptococcus pyogenes
US-09-494-297-1
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Query Match 100.0%; Score 2274; DB 5; Length 2274;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atgaaaaaacaagtttccaaataagcttaacttaatactcaagaaggtatga 60
DB 1 atgaaaaaacaagtttccaaataagcttaacttaatactcaagaaggtatga 60

QY 61 aaaaactcaaacgattactgtcaacttaagtggaagcttttaatagtctcgcttg 120
DB 61 aaaaactcaaacgattactgtcaacttaagtggaagcttttaatagtctcgcttg 120

QY 121 gtaacttcaagtggtgtgtaagactgttttggttaagtagaatccctgaagcaaac 180
DB 121 gtaacttcaagtggtgtgtaagactgttttggttaagtagaatccctgaagcaaac 180

QY 181 gcaataaatccagattcaagttcgaatacagatggatgataatgaatctta 240
DB 181 gcaataaatccagattcaagttcgaatacagatggatgataatgaatctta 240

QY 241 gggcattcattataataacagtttagagtagacacagatttaagggttaacttaagaaga 300
DB 241 gggcattcattataataacagtttagagtagacacagatttaagggttaacttaagaaga 300

QY 301 agtagaagttataaagtttaagtttaacttaataaagaacatttcctcgcgataagat 360
DB 301 agtagaagttataaagtttaagtttaacttaataaagaacatttcctcgcgataagat 360

QY 361 agtagtgttaaaaaagtggtataaaaaacatgagatgactctcaaaatttgaagatt 420
DB 361 agtagtgttaaaaaagtggtataaaaaacatgagatgactctcaaaatttgaagatt 420
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QY 421 gcatgagccctagaaatcagggagatgagctaaatcagaagttaacagctgtatgat 480
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DB 421 gggatgagccctagaaatcagggagatgagctaaatcagaagttaacagctgtatgat 480
QY 481 aatgagcatccacaataatgccaatgcatatgaaagagcttggaaaccttgaaatgcatc 540
|||||
DB 481 aatgagcatccacaataatgccaatgcatatgaaagagcttggaaaccttgaaatgcatc 540
QY 541 aagatgtaacaaagagcggtatgtagtactatctcgtaaatgctcctatcttaacagat 600
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DB 541 aagatgtaacaaagagcggtatgtagtactatctcgtaaatgctcctatcttaacagat 600
QY 601 gaaagttttaaagaggagcagaagaatgagttagtagtactcctcaatcttcttgatg 660
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DB 601 gaaagttttaaagaggagcagaagaatgagttagtagtactcctcaatcttcttgatg 660
QY 661 cgtcaagcttgaagcaactgtagtaccgaatttggcaactaaatgccaataaacaagt 720
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DB 661 cgtcaagcttgaagcaactgtagtaccgaatttggcaactaaatgccaataaacaagt 720
QY 721 cggagatgattcagtagtattttttagtctcggagacaaggagataataataa 780
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DB 721 cggagatgattcagtagtattttttagtctcggagacaaggagataataataa 780
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DB 841 ccaaccaatgctccaaatcacaactcacaagactcagtagtacttaataagaagtctata 900
QY 901 ggtgtaactcctaaatctgttgaaggctgcaactttagcagttgcaaggagataacgtg 960
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DB 901 ggtgtaactcctaaatctgttgaaggctgcaactttagcagttgcaaggagataacgtg 960
QY 961 agtttcaagcgagagtggtttagcagtaatgtagatgagaaagaaatgaactatagat 1020
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DB 961 agtttcaagcgagagtggtttagcagtaatgtagatgagaaagaaatgaactatagat 1020
QY 1021 ggaactatacttaactgaatgaattcctcagctggttatagtatcgagagccaatc 1080
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QY 1081 actttaaaggttgaagctgagcaagtgtagtactatgtagtgaagaaacagatggaat 1140
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DB 1081 actttaaaggttgaagctgagcaagtgtagtactatgtagtgaagaaacagatggaat 1140
QY 1141 cccaataaagagatagtagagccttactcagtagaagcatatatagttttgaagattt 1200
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DB 1141 cccaataaagagatagtagagccttactcagtagaagcatatatagttttgaagattt 1200
QY 1201 agcgttttaactacacaaactatgcaaaatttattatgcaaaaaataaaatggaagt 1260
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DB 1201 agcgttttaactacacaaactatgcaaaatttattatgcaaaaaataaaatggaagt 1260
QY 1261 tcaacaggttgcattgctttaaagtagcagatctaaatctccacagaccttgaaagtgt 1320
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DB 1261 tcaacaggttgcattgctttaaagtagcagatctaaatctccacagaccttgaaagtgt 1320
QY 1321 gggaaacaatgagctcagacttacaacagagaaagtaaatatatactatgtagagt 1380
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DB 1321 gggaaacaatgagctcagacttacaacagagaaagtaaatatatactatgtagagt 1380
QY 1381 cgtgaccttttaataatactgtgaaacaaagagataccgattcctgaactttcttaaaa 1440
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DB 1381 cgtgaccttttaataatactgtgaaacaaagagataccgattcctgaactttcttaaaa 1440
QY 1441 catatcaaaaagtaattgagaaagggttacaaggaaagaaagcaactatgtagtagt 1500
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DB 1441 catatcaaaaagtaattgagaaagggttacaaggaaagaaagcaactatgtagtagt 1500
QY 1501 ggtctaacgagacacaaatgctgcgtagtactcagttagcaatatatattcactgat 1560
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DB 1501 ggtctaacgagacacaaatgctgcgtagtactcagttagcaatatatttccactgat 1560
QY 1561 agtgcgttaattgataagagataaactaaagactatcaatggttttggagacttgatgat 1620
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DB 1561 agtgcgttaattgataagagataaactaaagactatcaatggttttggagacttgatgat 1620
QY 1621 agtacttaagcagttgctaaatccctgtgagataacgctcaagatagtaatccccaag 1680
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DB 1621 agtacttaagcagttgctaaatccctgtgagataacgctcaagatagtaatccccaag 1680
QY 1681 ctaactgaccttgatcttcttactcgcgaataaacaataatcaatcttcttgaact 1740
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DB 1681 ctaactgaccttgatcttcttactcgcgaataaacaataatcaatcttcttgaact 1740
QY 1741 cagtggtcaccagaagatttagtataatctgtagatgagaaagaaagaaagttata 1800
|||||
DB 1741 cagtggtcaccagaagatttagtataatctgtagatgagaaagaaagaaagttata 1800
QY 1801 cctgtactcataatttaacattgagaaacggtgactggttagctgtgtacagaaact 1860
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DB 1801 cctgtactcataatttaacattgagaaacggtgactggttagctgtgtgtacagaaact 1860
QY 1861 aagatctccatttgaatgaaatgaaataaataaagcaagatgcttctcaact 1920
|||||
DB 1861 aagatctccatttgaatgaaatgaaataaataaagcaagatgcttctcaact 1920
QY 1921 gtttaaacagataaaccaactcgaatttaagaatgtagaaagcaaccattatataa 1980
|||||
DB 1921 gtttaaacagataaaccaactcgaatttaagaatgtagaaagcaaccattatataa 1980
QY 1981 catgggaaagtttaaacattcaaggtttacagaaggttattcctacttgcataaga 2040
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DB 1981 catgggaaagtttaaacattcaaggtttacagaaggttattcctacttgcataaga 2040
QY 2041 acagattctgaaggttaaggttaagtttaagtaagcaagaagttagcaatgctcagtt 2100
|||||
DB 2041 acagattctgaaggttaaggttaagtttaagtaagcaagaagttagcaatgctcagtt 2100
QY 2101 tcaaaaacagagataaagaatgtagtagacattgcttggaaataaataaagaagcgtgt 2160
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DB 2101 tcaaaaacagagataaagaatgtagtagacattgcttggaaataaataaagaagcgtgt 2160
QY 2161 gttcctacagaggttgcataaagaatcaatgtagtagccttgcagtagtagttagtgcgtgt 2220
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DB 2161 gttcctacagaggttgcataaagaatcaatgtagtagccttgcagtagtagttagtgcgtgt 2220
QY 2221 atcagtttgggagcttggggaattcacaacgataagagataagaacaatgactag 2274
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RESULT 2
US-09-494-297-3
; Sequence 3, Application US/09494297
; GENERAL INFORMATION:
; APPLICANT: PODBIELSKI, ANDREAS
; TITLE OF INVENTION: COLLAGEN-BINDING PROTEINS FROM STREPTOCOCCUS PYOGENES
; FILE REFERENCE: P06628US0/BAS
; CURRENT APPLICATION NUMBER: US/09/494,297
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 2229
; TYPE: DNA
; ORGANISM: Streptococcus pyogenes
US-09-494-297-3

Query Match 31.7%; Score 720.8; DB 5; Length 2229;
Best Local Similarity 61.6%; Pred. No. 3.3e-140;
Matches 1372; Conservative 0; Mismatches 787; Indels 69; Gaps 11;

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Db	40	aaccaaagcaagaacaaacgagatccggtattactctgaagaagtcttttaacgtttgtagctcg	99
OY	121	gtaaactccatgtgtgtgtgtaagactggttttggtttaagtaagaatccctgacgcgaac	180
Db	100	atagaatagtagggctttgtttctcaacagagcgctccgagctgtgaagaacaaatcgtaacaa-	158
OY	181	gcaataaatccagatctcaaatctcggaataacagatgtaatgtaataatctatgtaaga	240
Db	159	-----tagacaaagctcaaatccaagtattccgtgtgtaagtcgtatgattcttaacctaa	213
OY	241	gggataccatattataaaacggtttagtaglacacacgatttaaggttaacttgaaga	300
Db	214	ggataccagacatcatgctccgtttaaagacttccaaatatttaaaagtaattttagggga	273
OY	301	agtaagaattatccaagtttatgtcttaatttaagaagaacattccctccgtgcacat	360
Db	274	agtaagaattatccaagtttatgtcttaatttaagaagaacattccctccgtgcacat	333
OY	351	agtcagtttaaaaaagttgtaataaaaaacatgtagtaactctcaaaaatttgaagatat	420
Db	334	agttttatgatacaaatgtgtaataaaaacttggaaaggaacttaagaaacttatacaagta	393
OY	421	ggcgtgagcccttgaattacagagagatggcgtaaatcagaagttaacggtcgttatgat	480
Db	394	gcagataaacccaagaatagagaagcaggttacaacaaaataatattgagattcccat	453
OY	481	aatgagatacccaaaaatgccaatggttatattagagaagcttggaaacccgttaatgctatc	540
Db	454	aatgataatccataatcatgtaatggttaatgaaagagatagatcccttaaacgatt	513
OY	541	agaattacacaagaagcggtatggtactcttctgtaatagcccatcttcaatccgat	600
Db	514	ttatgctcccaaatgctcatltgtgt-----taacgataccgcgccaatccaatccgat	567
OY	601	gaaagtttlaaaagggaagtcagaagaataacttggtagtaactccaattactcttgg	660
Db	568	gaaagtttlaaaacagaagtcgtaagtaatgtaattgaatgacacagcagttggttaagt	627
OY	661	cgtcaagcctttgaagccaactgtagtaccgaatttggccaactaaatgcacaacaagt	720
Db	628	cgaaaagcttlaaaagggaacttatgtctccaactttaggttccaataattcgaataaaact	687
OY	721	ccgagatatttccagcaagtatatttggctcgtcgagacaagaaggatataataataa	780
Db	688	ccatcaggttatcgtttaaagtattgtaattgtaattcatgatgaagcct-----	732
OY	781	ggaatacaaaaactttttagttggttggtttagttccbaactaaaccaactccaggaag	840
Db	733	---ttccaaaactttttagttggttggttggttccgatactccccaacaaacaggaga-	788
OY	841	ccacaatgctccaaataactcaactccaagacttaagtaactattagaagtatgctata	900
Db	789	-----agagctcccggtcaaaaacttgaaaaaacatacaagtcacgtatataagaataatgcgga	843
OY	901	ggttattaccctaaatttgccttgaaggtgaacatacagttgacacggggataacgttgat	960
Db	844	ggtgt---accttaaaactcttagggggaggaacacttaagctttcccaaattggaagagt	900
OY	961	agtttcaagcggaggtgttttagcagtaatgtaatttggaagaagaattggaactacagat	1020
OY	1021	ggaactatcttacttaacttgaattggaatttccagcgtggttatagtatcgagagccaatc	1080
Db	961	ggagcttatacttcaacagaagaacatactccagatggaataaaaattgcggagccgatt	1020
OY	1081	actttaagttgaagctgcgaagtgtatactat--tattatgtaaaaaacagattgaa	1137
Db	1021	aagtttaggtatagaataataaaaagatttacttgcgtccaaaagaagatggtttcccaadtgaa	1080

QY	1138	aatcccaataaagagatagtagagccttactcagtagaagcaataatgatgtt---gaa	1194
Db	1081	aatcccaataaagagatagtagagcctaactcagtagaagcgatataatgatcttatgat	1140
QY	1195	gaatttagcggtttaaactatacaacaacatagcaaaattttattatagcaaaaaataaaat	1254
Db	1141	gaagaagtaactctcgggttctaactccaatagcaaaattctatacgtcatacaataatgat	1200
QY	1255	ggaagtccaagcgtctgctctatcttgctttaaacygaactaataatcccaacagactgaa	1314
Db	1201	aaaagtccaagcgtctgctctactcgtctcctaagcgtgatttaactccaacactgaccat	1260
QY	1315	gatggtggaaaaacaatgatctcaga---cttaacaacagsgaagtaaaatacaatcat	1371
Db	1261	gatagtggtggaactataaataccagatactatgatacgatgaagaagtcagatacacat	1320
QY	1372	atgcagtgctgtagcccttataatatactcgtgaaacccaagatataccgatccctgacac	1431
Db	1321	acggacagtgtagctctgtttaaatalgctgaagcccgagsgatacataatccgaagac	1380
QY	1432	ttcttaaaacatacaaaaagaatattggaaggggtacaagggaanaagacaagctat	1491
Db	1381	ttcttaaaagccactaaaanaagtaattggaanaagcgtacaagaaaaaagg-----gat	1454
QY	1492	gagatagtggtctaactgtagacacaatlgcgtgcggtactcagtltagcaatatbat	1551
Db	1435	agcataatgatttaacagaacaacagatttcgsgcgtactcagcttgctctattat	1494
QY	1552	ttcaactgatgtctgtaattaga-----taagataaactaaagaactatcat	1599
Db	1495	tttacaagcagtgctgctttaaaaaccttaaaaactttaaaaagtggaaggtatccat	1554
QY	1600	ggttttggaagacagtaatgtagtactttagacggttgcgtcaaatccctgtgtagaagct	1659
Db	1555	ggatttgtaactatagtgatgtaaaaaaacccctcagctgtcacaaaagaattatacttatg	1614
QY	1660	caagataagtaactccccaacagctactgaactgtatcttatttcgataatacaataaa	1719
Db	1615	caaatgycagtgccctccaactaacaataatctgatttcttcgtacctaaataagcaaa	1674
QY	1720	tatcaatctcttatgtgaactcagtgcatccagaagatttagttgatatatttcggtatg	1779
Db	1675	gaccaatctcttatgttggaacagatgccaaccagatgatttggtgacgtgattcgtatg	1734
QY	1780	gaagataaaa---aagaagtataacctgtaaaccaatatttaacattgagaanaacggtg	1836
Db	1735	gaagataaaaagcagaagaattatccaagttaactccaagtttgcacggtgaaaaaaacgta	1784
QY	1837	actggtttagctgtgtgacagaaactaaagaatttccatttgaattgaaatltaaaaaat	1896
Db	1795	gtcgtgtgagttgggaagataaactaaagaagtttccaatttgaaacttgagttgaagataa	1854
QY	1897	aagcaagaattgcttcttcaaaactgtttaaacaagataaaaacaacactcogaattaaag	1956
Db	1855	actgacagacctattgtttaaacactcttaaaaactaaataatcaagatttagtactaaag	1914
QY	1957	ggttaagaacacatttaattttaaanaacgtgggaagtttaacgcttcaggttttaccagaa	2016
Db	1915	gggaataattcaatttaacttaaaagcagatvggacacataagaattagaagattaccagc	1974
QY	2017	ggttattcttactctgtgcaaaagaacaagattctcgaaagcgctataaagtttaaaagttaag	2076
Db	1975	ggatattcttatactcgtgaagaagcgtcgaagcgaagtataatagttaacggttgataac	2034
QY	2077	caagaagttagcaaatgctacagtttcaaaaaacaggaataacaagtgtatgagacactgtc	2136
Db	2035	aaagtgtagtcaagaagcgcagtcagtagtgaagataatacagaagaacaaaagctact	2094
QY	2137	tttgaataataataaaggcctgtgttcttcacagsggtgtgaccaagaatcaatgagcat	2196
Db	2095	cttgaaaaccgaaaagctctgtgccaacaacggtgttgacaacagatgvggctatctat	2154
QY	2197	ctagctttgatagtatacgcgtgtgtatcagtttggtggatcttggtggaattccaacagataag	2256

Query Match 2.1%; Score 48.6; DB 6; Length 69513;
Best Local Similarity 49.9%; Pred. No. 0.55;
Matches 179; Conservative 0; Mismatches 174; Indels 6; Gaps 2;

QY 1694 attcttcttcggaatacaataatcatctcttattggaactcagtggaatcag 1753
DB 61670 ATTAAATATTTCTTACGTATTTAAATTTAAATTTAAATTTAAATTTAA 61611

QY 1754 aagatttagttgattatctgtaagagaataaagaagttatacctgtaacta 1813
DB 61610 AAATTTTAATTT-TTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTTA 61552

QY 1814 atttaacattgagaaacagtgactggttttaagctgtaagacagaaagattccatt 1873
DB 61551 ATTTAATATTGAGGCAAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAA 61492

QY 1874 ttgaaatttgaaataaataaataaataaataaataaataaataaataaataa 1933
DB 61491 TTAAATATTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAA 61432

QY 1934 aaacaacactggaatttaagatgtaagcaac-----attaatttaaacatgagga 1988
DB 61431 AAATTAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTTA 61372

QY 1989 aagtttaacactcaaggtttaccagaaggtttcttaccctgtaagaagaacagatt 2047
DB 61371 AAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTT 61313

RESULT 6
US-09-739-449-1234/C
; Sequence 1234, Application US/09739449
; GENERAL INFORMATION:
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15490)C
; CURRENT APPLICATION NUMBER: US/09/739,449
; CURRENT FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: US 09/514,000
; PRIOR FILING DATE: 2000-02-23
; NUMBER OF SEQ ID NOS: 13351
; SEQ ID NO 1234
; LENGTH: 753
; TYPE: DNA
; ORGANISM: Agrobacterium tumefaciens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)-(753)
; OTHER INFORMATION: unsure at all n locations
US-09-739-449-1234

Query Match 2.1%; Score 47.8; DB 5; Length 753;
Best Local Similarity 36.4%; Pred. No. 0.33;
Matches 160; Conservative 0; Mismatches 279; Indels 0; Gaps 0;

QY 1761 agttgatattatctgtaagagaataaagaagttatacctgtaactcataattaac 1820
DB 723 ATTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTT 654

QY 1821 attgagaaacagtgactggttttaagctgtaagacagaaagattccatttgaat 1880
DB 663 AAATAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAA 604

QY 1881 tgaatttaaaaaataaagaagaattgcttctcaaacgttcaaaacagataaacaacaa 1940
DB 603 AAATAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAA 544

QY 1941 cctcgaatttaagatgtaagcaacatttaatttaaacatgaggaagtttaacact 2000
DB 543 AAATAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAA 484

QY 2001 tcaaggtttcagaaggttattcttacccttgcaagaacacagattctgaagctataa 2060
DB 483 AAATAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAA 424

QY 2061 ggttaagttataagcaagaagtaagcaaatgctacagtttcaaaaacaggaatacaag 2120
DB 423 AATTTAANNNAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNA 364

QY 2121 tgaatgacactgcttcttgaaataataaagaagcctgtgttccctcagaaggtatca 2180
DB 363 NNN 304

QY 2181 aaagatcaatgctacta 2199
DB 303 NNN 285

RESULT 7
US-09-739-449-2256/C
; Sequence 2256, Application US/09739449
; GENERAL INFORMATION:
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15490)C
; CURRENT APPLICATION NUMBER: US/09/739,449
; CURRENT FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: US 09/514,000
; PRIOR FILING DATE: 2000-02-23
; NUMBER OF SEQ ID NOS: 13351
; SEQ ID NO 2256
; LENGTH: 834
; TYPE: DNA
; ORGANISM: Agrobacterium tumefaciens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)-(834)
; OTHER INFORMATION: unsure at all n locations
US-09-739-449-2256

Query Match 2.1%; Score 47.8; DB 5; Length 834;
Best Local Similarity 43.9%; Pred. No. 0.34;
Matches 196; Conservative 0; Mismatches 250; Indels 0; Gaps 0;

QY 1708 aatacaataaataatcaatcttattggaactcagtgcatccagaagaatttagttgat 1767
DB 660 AATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 601

QY 1768 attatcgtatggaagataaagaagaattatacctgtaactcataatttaacattgaga 1827
DB 600 AAATAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAA 541

QY 1828 aaaaagtgactggttttagctgtaagacagaaagattccatttgaattgaatta 1887
DB 540 AAATAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAA 481

QY 1888 aaaaataaataaagaagaattgcttctcaaacgtttaaacaagataaacaacactcgaa 1947
DB 480 AAATAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAA 421

QY 1948 tttaagaatgtaagcaacatttaatttaaacatgaggaagtttaacactcaagct 2007
DB 420 AAATAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAA 361

QY 2008 ttacagaaggttattcttacccttgcaagaacagattctgaagctataaggttaaa 2067
DB 360 AAATAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAA 301

QY 2068 gtttaatagccaagaagtaagcaaatgctacagtttcaaaaacaggaataaacaagttgat 2127
DB 300 AAATAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAA 241

QY 2128 acacttccttgaataataaga 2153
 Db 240 CCGCCCCCCCCCAAAAAAAAAA 215

RESULT 8

US-08-956-171C-320
 ; Sequence 320, Application US/08956171C
 ; GENERAL INFORMATION:
 APPLICANT: Charles Kunsch
 Gil H. Choi
 Patrick S. Dillon
 Craig A. Rosen
 Steven C. Barash
 Michael R. Fannon

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
 NUMBER OF SEQUENCES: 5255
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Human Genome Sciences, Inc.
 STREET: 9410 Key West Avenue
 CITY: Rockville
 STATE: Maryland
 COUNTRY: USA
 ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 Inch, 1.4MB storage
 COMPUTER: HP Vectra 486/33
 OPERATING SYSTEM: MSDOS version 6.2
 SOFTWARE: ASCII Text
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/956,171C
 FILING DATE: 20-Oct-1997
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/009,861
 FILING DATE: January 5, 1996
 APPLICATION NUMBER: 08/781,986
 FILING DATE: January 3, 1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Hoover, Kenley K.
 REGISTRATION NUMBER: 40,302
 REFERENCE/DOCKET NUMBER: PB248P1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (301) 610-5790
 TELEFAX: (301) 309-8439
 INFORMATION FOR SEQ ID NO: 320:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5897 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear

US-08-956-171C-320
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 320:

Query Match 2.1%; Score 47.4; DB 4; Length 5897;
 Best Local Similarity 46.3%; Pred. No. 0.6; Indels 0; Gaps 0;
 Matches 156; Conservative 0; Mismatches 181;

QY 865 caaacactcgaactcttgaagaagtctgctagtgatgattactctaattgcttga 924
 Db 4351 CCAATATATTCGATTAGATTGTAATCAAAAAGAAAGTAATCAATTTTGAATTATTT 4410
 QY 925 ggtgcacattacagttgcaggggataacgltgaatgatttcaagcgaagtgcttga 984
 Db 4411 GATGAATCATTTATTCGTAAGAGTAGATGAACTTTTATCAAGAGTCTCTCAATTA 4470
 QY 985 agtaagatagatggagaagaatgaaactacatcgatggaactatacttaactgaatg 1044
 Db 4471 ATTAAATGAATAAAGAAAGAGCCATGATGTTTATTTTGAATTTAAACGATGATATT 4530
 QY 1045 aattccacgctggtatagatcagcagagccatcatttaaggttgaagctgcaaa 1104

Db 4531 CCTAATACAGTTGGTAAGCGCATGAAGACTAGCTAATTAATGATGATCGTAAT 4590
 QY 1105 ggtatatacatattatgtgaaacacagattgaaatcccaataaagagatagagcct 1164
 Db 4591 GTTCATGCTGCTGCTGCGCTAAATAATGATGCTGAGCCATTAAAGATTAAAGAAACAT 4650
 QY 1165 tactcagtagaagacataatgatttgaagaattta 1201
 Db 4651 AATCAAGATACAAAATTTATTCAGTAAACACAGCTTA 4687

RESULT 9

US-09-739-449-1953
 ; Sequence 1953, Application US/09739449
 ; GENERAL INFORMATION:
 APPLICANT: Hinkle, Gregory J.
 APPLICANT: Slater, Steven C.
 TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
 FILE REFERENCE: 38-10(15490)C
 CURRENT APPLICATION NUMBER: US/09/739,449
 CURRENT FILING DATE: 2000-12-19
 PRIOR APPLICATION NUMBER: US 09/514,000
 PRIOR FILING DATE: 2000-02-23
 NUMBER OF SEQ ID NOS: 13351
 SEQ ID NO 1953
 LENGTH: 1131
 TYPE: DNA
 ORGANISM: Agrobacterium tumefaciens
 FEATURE:
 NAME/KEY: unsure
 LOCATION: (1)..(1131)
 OTHER INFORMATION: unsure at all n locations
 US-09-739-449-1953

Query Match 2.1%; Score 47.2; DB 5; Length 1131;
 Best Local Similarity 44.1%; Pred. No. 0.48;
 Matches 163; Conservative 0; Mismatches 207; Indels 0; Gaps 0;

QY 1781 aagataaaaaagaagtatacctgttaactcataatattaacattgagaaaaagtgactg 1840
 Db 510 aaaaaaaanaaaaaaanaaaaaaanaaaaaaanaaaaaaanaaaaaaanaaaaaa 569
 QY 1841 gttgactggtgcagacttaagatttcatttgaattgaattgaattgaattgaattga 1900
 Db 570 nnaaaaaaanaaaaaaanaaaaaaanaaaaaaanaaaaaaanaaaaaaanaaaaaa 629
 QY 1901 aagaattgcttcgaactgtttaaacagataaaacaaactcgaaatttaagaatgta 1960
 Db 630 aaaaaaaanaaaaaaanaaaaaaanaaaaaaanaaaaaaanaaaaaaanaaaaaa 689
 QY 1961 aagcaacattaatttaaacatggtgaagtttaacacttaaggttaccagaaggtt 2020
 Db 690 aaaaaaagaanaaaaaaagaanaaagaanaaagaanaaagaanaaagaanaaagaana 749
 QY 2021 attcttacttgcagaagaacagattctgaagtcataagtttaagtttaagttgaag 2080
 Db 750 aaaaaaaanaaaaaaanaaaaaaanaaaaaaanaaaaaaanaaaaaaanaaaaaa 809
 QY 2081 aagtagcaatgctacagtttcaaacacggaataaacaagtatgagacactgctttg 2140
 Db 810 aagaaagcaanagaagagaaaaaanaaagaagaagaagaagaagaagaagaagaaga 869
 QY 2141 aaaaataata 2150
 Db 870 aaaaaaanaa 879

RESULT 10
 US-09-739-449-8012
 ; Sequence 8012, Application US/09739449
 ; GENERAL INFORMATION:
 APPLICANT: Hinkle, Gregory J.

```

RESULT 12
US-09-663-882-1
; Sequence 1, Application US/09663882
; GENERAL INFORMATION:
; APPLICANT: MacInga, David R.
; TITLE OF INVENTION: Counter-selection vector for gram positive bacteria
; FILE REFERENCE: ID01008 US
; CURRENT APPLICATION NUMBER: US/09/663, 882
; CURRENT FILING DATE: 2001-09-15
; PRIOR APPLICATION NUMBER: US 60/154, 694
; PRIOR FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1

```

```
; SEQ ID NO 1
; LENGTH: 2850
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1355)..(2047)
; NAME/KEY: RBS
; LOCATION: (1344)..(1349)
; NAME/KEY: -10_signal
; LOCATION: (1302)..(1307)
; NAME/KEY: -35_signal
; LOCATION: (1281)..(1284)
; US-09-663-882-1
```

Query Match 2.0%; Score 46; DB 5; Length 2850;

Best Local Similarity 47.0%; Pred. No. 1;

Matches 142; Conservative 0; Mismatches 160; Indels 0; Gaps 0;

```
QY 865 caaacgactcagctactattagaagaatgctatgctatgctacttaattgctgaa 924
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1370 ccaattctcattagatttctgaatcaaaagaataatcaattttagatttatt 1429
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 925 ggtgcaacttacagttgacaggggatacgtgatagttttcaagcgagagtgtagc 984
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1430 gataaatacattatcgtaaaagtgatgtaagtaactttttatcaagaagtcctcaatta 1489
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 985 agtaaatatcttgagaagaatgtaactcagatcgaaacttaacttaactgaattg 1044
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1490 ataatgagataaagaagaagagcgcatgattttagatttaaaacgcatgatact 1549
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1045 aattctcagctggttagttagtcgagagcgaactctttaaggttgagctggcaaa 1104
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1550 cctaatacagctggtgaagcgatggaagcactgaattgaattgctgtaaat 1609
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1105 gctatacttcttctgtaaaacagatgaaatcccaataaagagatagtagcct 1164
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1610 gtcatgctgctggtggtgcaaaatgatgtctgagggccattaaagattaaagaacat 1669
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1165 ta 1166
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1670 aa 1671
```

RESULT 13

```
US-09-739-449-1859/C
; Sequence 1859, Application US/09739449
; GENERAL INFORMATION:
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15490)C
; CURRENT APPLICATION NUMBER: US/09/739,449
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: US 09/514,000
; PRIOR FILING DATE: 2000-02-23
; NUMBER OF SEQ ID NOS: 13351
; SEQ ID NO 1859
; LENGTH: 1250
; TYPE: DNA
; ORGANISM: Agrobacterium tumefaciens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(1250)
; OTHER INFORMATION: unsure at all n locations
; US-09-739-449-1859
```

Query Match 2.0%; Score 45.6; DB 5; Length 1250;

Best Local Similarity 33.4%; Pred. No. 1;

Matches 204; Conservative 0; Mismatches 407; Indels 0; Gaps 0;

```
QY 1543 atattattcactgtagtgcgtaattagataagaataactaaagactatcatgct 1602
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1181 AAAAAAAAAAATTTAAAAAATAAAAAAAAAAAAAAAAAA 1122
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1603 ttgagacatagatagtactttagcagctgtctaaatcctgtgagatacgtcaa 1662
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1121 AAAAAAAAAAATTTAAAAAATAAAAAAAAAAANNAANNAANNAANNAANNA 1062
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1663 gatagtatccctccagcgtcaactgactgattctttatccgataaataatatt 1722
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1061 NNNNAATTTAANNAAAAAAAAAANNNNNNNAANNAANNAANNAANNAANNN 1002
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1723 caatctcttattggaactcagtgcatccagaagatttagtatacttcgtatgaa 1782
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1001 AAAAAAAAAAATAAAAAAAAAAANNAANNAANNAANNAANNAANNAANNA 942
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1783 gataaaagaagttatacctgtaactcataattaacattgagaaaacgctgactgct 1842
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 941 AAAAAAAAAAANNNNNNAANNAANNAANNAANNAANNAANNAANNAANNA 882
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1843 ttgctggtgacagaaacttaagattccatttgaattgaattgaataaataatagcaa 1902
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 881 ANNAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNA 822
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1903 gaattgcttctcaactgtaaaacagataaaacaactcgatttaagaatgtaaa 1962
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 821 AANNAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNA 762
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1963 gcaaccataattaaacaatgaggaaagttaaacacttaaggttaccagaagttat 2022
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 761 AAAAAAAAAAANNAANNAANNAANNAANNAANNAANNAANNAANNA 702
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2023 tcttactcttcaagaagaagattctgaagctataaggttaagttatagcagaag 2082
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 701 NNNNAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNA 642
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2083 gtagcaatgctacagtttcaaaacagagaatacaagttgatgacactgcttgaa 2142
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 641 AAAAAAAAAAATAAAAAAAAAAANNAANNAANNAANNAANNAANNAANNA 582
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2143 aataataaga 2153
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 581 AAAAAAAAAA 571
```

RESULT 14

```
US-08-956-171C-177
; Sequence 177, Application US/08956171C
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; APPLICANT: Gil H. Chol
; APPLICANT: Patrick S. Dillon
; APPLICANT: Craig A. Rosen
; APPLICANT: Steven C. Barash
; APPLICANT: Michael R. Fannon
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/956,171C
; FILING DATE: 20-Oct-1997
; CLASSIFICATION: <Unknown>
```


